



SEQUENCE LISTING

<110> Bruck, Claudine
Bollen, Alex
Jacobs, Paul
Massaer, Marc

<120> Recombinant Allergen with Reduced
Enzymatic Activity

<130> B45122

<140> 09/554,860

<141> 2000-05-19

<150> PCT/EP98/07521

<151> 1998-11-16

<150> GB 9724531.0

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<211> 963

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<213> Artificial Sequence

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<223> Mutant of DerP1

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gcctgcagta tcaatggaaa tgctccagct gaaatcgatt tgcgacaaat gcgaactgtc 360
actcccattc gtatgcaagg aggctgtggt tcagcttggg ctttctctgg tgttgccgca 420
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			20					25					30		
Phe	Asn	Lys	Ser	Tyr	Ala	Thr	Phe	Glu	Asp	Glu	Glu	Ala	Ala	Arg	Lys
		35					40					45			
Asn	Phe	Leu	Glu	Ser	Val	Lys	Tyr	Val	Gln	Ser	Asn	Gly	Gly	Ala	Ile
	50					55					60				
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65					70					75					80
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				85					90					95	
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Asp	Leu	Arg	Gln	Met	Arg	Thr	Val	Thr	Pro	Ile	Arg	Met	Gln	Gly	Gly
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Cys	Gly	Ser	Ala	Trp	Ala	Phe	Ser	Gly	Val	Ala	Ala	Thr	Glu	Ser	Ala
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Tyr	Leu	Ala	Tyr	Arg	Asn	Gln	Ser	Leu	Asp	Leu	Ala	Glu	Gln	Glu	Leu
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Phe	Gly	Ile	Ser	Asn	Tyr	Cys	Gln	Ile	Tyr	Pro	Pro	Asn	Val	Asn	Lys
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Ile	Arg	Glu	Ala	Leu	Ala	Gln	Thr	His	Ser	Ala	Ile	Ala	Val	Ile	Ile
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			245					250						255	
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			260					265					270		
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	275						280					285			
Ser	Trp	Asp	Thr	Asn	Trp	Gly	Asp	Asn	Gly	Tyr	Gly	Tyr	Phe	Ala	Ala
	290					295					300				
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atgagtgcag aagcttttga acacctcaaa actcaattcg atttgaacgc ctgcagtatc 300
aatggaaatg ctccagctga aatcgatttg cgacaaatgc gaactgtcac tcccattcgt 360
atgcaaggag gctgtgggtc atgttgggtt ttctctggtg ttgccgcaac tgaatcagct 420
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<223> Mutant of DerP1

<400> 4

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Phe Asn Lys Ser Tyr Ala Thr Phe Glu Asp Glu Glu Ala Ala Arg Lys
35     40     45
Asn Phe Leu Glu Ser Val Lys Tyr Val Gln Ser Asn Gly Gly Ala Ile
50     55     60
Asn His Leu Ser Asp Leu Ser Leu Asp Glu Phe Lys Asn Arg Phe Leu
65     70     75     80
Met Ser Ala Glu Ala Phe Glu His Leu Lys Thr Gln Phe Asp Leu Asn
85     90     95
Ala Cys Ser Ile Asn Gly Asn Ala Pro Ala Glu Ile Asp Leu Arg Gln
100    105    110
Met Arg Thr Val Thr Pro Ile Arg Met Gln Gly Gly Cys Gly Ser Cys
115    120    125
Trp Ala Phe Ser Gly Val Ala Ala Thr Glu Ser Ala Tyr Leu Ala Tyr
130    135    140
Arg Asn Gln Ser Leu Asp Leu Ala Glu Gln Glu Leu Val Asp Cys Ala
145    150    155    160

Ser Gln His Gly Cys His Gly Asp Thr Ile Pro Arg Gly Ile Glu Tyr
165    170    175
Ile Gln His Asn Gly Val Val Gln Glu Ser Tyr Tyr Arg Tyr Val Ala
180    185    190
Arg Glu Gln Ser Cys Arg Arg Pro Asn Ala Gln Arg Phe Gly Ile Ser
195    200    205
Asn Tyr Cys Gln Ile Tyr Pro Pro Asn Val Asn Lys Ile Arg Glu Ala
210    215    220
Leu Ala Gln Thr His Ser Ala Ile Ala Val Ile Ile Gly Ile Lys Asp
225    230    235    240

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Leu	Asp	Ala	Phe	Arg	His	Tyr	Asp	Gly	Arg	Thr	Ile	Ile	Gln	Arg	Asp
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			260					265					270		
Asn	Ala	Gln	Gly	Val	Asp	Tyr	Trp	Ile	Val	Arg	Asn	Ser	Trp	Asp	Thr
		275					280					285			
Asn	Trp	Gly	Asp	Asn	Gly	Tyr	Gly	Tyr	Phe	Ala	Ala	Asn	Ile	Asp	Leu
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 ggaggtgccca tcaaccattt gtccgatttg tcggttgatg aattcaaaaa ccgattttttg 240
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 tgccgacgac caaatgcaca acgtttcggg atctcaaaact attgccaaat ttaccaccca 660
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 20 25 30
 Phe Asn Lys Ser Tyr Ala Thr Phe Glu Asp Glu Glu Ala Ala Arg Lys
 35 40 45
 Asn Phe Leu Glu Ser Val Lys Tyr Val Gln Ser Asn Gly Gly Ala Ile
 50 55 60

Asn	His	Leu	Ser	Asp	Leu	Ser	Leu	Asp	Glu	Phe	Lys	Asn	Arg	Phe	Leu
65					70					75					80
Met	Ser	Ala	Glu	Ala	Phe	Glu	His	Leu	Lys	Thr	Gln	Phe	Asp	Leu	Asn
				85					90					95	
Ala	Glu	Thr	Asn	Ala	Cys	Ser	Ile	Asn	Gly	Asn	Ala	Pro	Ala	Glu	Ile
			100					105					110		
Asp	Leu	Arg	Gln	Met	Arg	Thr	Val	Thr	Pro	Ile	Arg	Met	Gln	Gly	Gly
		115				120						125			
Cys	Gly	Ser	Ala	Trp	Ala	Phe	Ser	Gly	Val	Ala	Ala	Thr	Glu	Ser	Ala
	130					135				140					
Tyr	Leu	Ala	Tyr	Arg	Asn	Gln	Ser	Leu	Asp	Leu	Ala	Glu	Gln	Glu	Leu
145					150					155					160
Val	Asp	Cys	Ala	Ser	Gln	His	Gly	Cys	His	Gly	Asp	Thr	Ile	Pro	Arg
				165				170						175	
Gly	Ile	Glu	Tyr	Ile	Gln	His	Asn	Gly	Val	Val	Gln	Glu	Ser	Tyr	Tyr
		180						185					190		
Arg	Tyr	Val	Ala	Arg	Glu	Gln	Ser	Cys	Arg	Arg	Pro	Asn	Ala	Gln	Arg
		195					200					205			
Phe	Gly	Ile	Ser	Asn	Tyr	Cys	Gln	Ile	Tyr	Pro	Pro	Asn	Val	Asn	Lys
	210					215					220				
Ile	Arg	Glu	Ala	Leu	Ala	Gln	Thr	His	Ser	Ala	Ile	Ala	Val	Ile	Ile
225					230					235					240
Gly	Ile	Lys	Asp	Leu	Asp	Ala	Phe	Arg	His	Tyr	Asp	Gly	Arg	Thr	Ile
			245					250						255	
Ile	Gln	Arg	Asp	Asn	Gly	Tyr	Gln	Pro	Asn	Tyr	Ala	Ala	Val	Asn	Ile
			260					265					270		
Val	Gly	Tyr	Ser	Asn	Ala	Gln	Gly	Val	Asp	Tyr	Trp	Ile	Val	Arg	Asn
		275					280					285			
Ser	Trp	Asp	Thr	Asn	Trp	Gly	Asp	Asn	Gly	Tyr	Gly	Tyr	Phe	Ala	Ala
	290					295					300				
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<223> Mutant of DerP1

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			20					25					30		
Ala	His	Ser	Ala	Phe	Ala	Ala	Asp	Pro	Arg	Pro	Ser	Ser	Ile	Lys	Thr
		35					40					45			
Phe	Glu	Glu	Tyr	Lys	Lys	Ala	Phe	Asn	Lys	Ser	Tyr	Ala	Thr	Phe	Glu
	50					55					60				
Asp	Glu	Glu	Ala	Ala	Arg	Lys	Asn	Phe	Leu	Glu	Ser	Val	Lys	Tyr	Val
65					70					75					80
Gln	Ser	Asn	Gly	Gly	Ala	Ile	Asn	His	Leu	Ser	Asp	Leu	Ser	Leu	Asp
			85						90					95	

Glu	Phe	Lys	Asn	Arg	Phe	Leu	Met	Ser	Ala	Glu	Ala	Phe	Glu	His	Leu
			100					105					110		
Lys	Thr	Gln	Phe	Asp	Leu	Asn	Ala	Cys	Ser	Ile	Asn	Gly	Asn	Ala	Pro
		115					120					125			
Ala	Glu	Ile	Asp	Leu	Arg	Gln	Met	Arg	Thr	Val	Thr	Pro	Ile	Arg	Met
		130					135					140			
Gln	Gly	Gly	Cys	Gly	Ser	Cys	Trp	Ala	Phe	Ser	Gly	Val	Ala	Ala	Thr
145					150					155					160
Glu	Ser	Ala	Tyr	Leu	Ala	Tyr	Arg	Asn	Gln	Ser	Leu	Asp	Leu	Ala	Glu
				165					170					175	
Gln	Glu	Leu	Val	Asp	Cys	Ala	Ser	Gln	His	Gly	Cys	His	Gly	Asp	Thr
			180						185					190	
Ile	Pro	Arg	Gly	Ile	Glu	Tyr	Ile	Gln	His	Asn	Gly	Val	Val	Gln	Glu
			195				200					205			
Ser	Tyr	Tyr	Arg	Tyr	Val	Ala	Arg	Glu	Gln	Ser	Cys	Arg	Arg	Pro	Asn
	210					215					220				
Ala	Gln	Arg	Phe	Gly	Ile	Ser	Asn	Tyr	Cys	Gln	Ile	Tyr	Pro	Pro	Asn
225						230				235					240
Ala	Asn	Lys	Ile	Arg	Glu	Ala	Leu	Ala	Gln	Thr	His	Ser	Ala	Ile	Ala
						245				250					255
Val	Ile	Ile	Gly	Ile	Lys	Asp	Leu	Asp	Ala	Phe	Arg	His	Tyr	Asp	Gly
			260					265						270	
Arg	Thr	Ile	Ile	Gln	Arg	Asp	Asn	Gly	Tyr	Gln	Pro	Asn	Tyr	His	Ala
			275				280						285		
Val	Asn	Ile	Val	Gly	Tyr	Ser	Asn	Ala	Gln	Gly	Val	Asp	Tyr	Trp	Ile
	290					295					300				
Val	Arg	Asn	Ser	Trp	Asp	Thr	Asn	Trp	Gly	Asp	Asn	Gly	Tyr	Gly	Tyr
305					310					315					320
Phe	Ala	Ala	Asn	Ile	Asp	Leu	Met	Met	Ile	Glu	Glu	Tyr	Pro	Tyr	Val
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Val	Ile	Leu													

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			20					25					30		
Ala	His	Ser	Ala	Phe	Ala	Ala	Asp	Pro	Arg	Pro	Ser	Ser	Ile	Lys	Thr
		35					40					45			
Phe	Glu	Glu	Tyr	Lys	Lys	Ala	Phe	Asn	Lys	Ser	Tyr	Ala	Thr	Phe	Glu
	50					55					60				
Asp	Glu	Glu	Ala	Ala	Arg	Lys	Asn	Phe	Leu	Glu	Ser	Val	Lys	Tyr	Val
65					70					75					80
Gln	Ser	Asn	Gly	Gly	Ala	Ile	Asn	His	Leu	Ser	Asp	Leu	Ser	Leu	Asp
				85					90					95	
Glu	Phe	Lys	Asn	Arg	Phe	Leu	Met	Ser	Ala	Glu	Ala	Phe	Glu	His	Leu
			100					105					110		

Lys Thr Gln Phe Asp Leu Asn Ala Glu Thr Asn Ala Cys Ser Ile Asn
 115 120 125
 Gly Asn Ala Pro Ala Glu Ile Asp Leu Arg Gln Met Arg Thr Val Thr
 130 135 140
 Pro Ile Arg Met Gln Gly Cys Gly Ser Ala Trp Ala Phe Ser Gly
 145 150 155 160
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 165 170 175
 Asp Leu Ala Glu Gln Glu Leu Val Asp Cys Ala Ser Gln His Gly Cys
 180 185 190
 His Gly Asp Thr Ile Pro Arg Gly Ile Glu Tyr Ile Gln His Asn Gly
 195 200 205
 Val Val Gln Glu Ser Tyr Tyr Arg Tyr Val Ala Arg Glu Gln Ser Cys
 210 215 220
 Arg Arg Pro Asn Ala Gln Arg Phe Gly Ile Ser Asn Tyr Cys Gln Ile
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 Tyr Pro Pro Asn Ala Asn Lys Ile Arg Glu Ala Leu Ala Gln Thr His
 245 250 255
 Ser Ala Ile Ala Val Ile Ile Gly Ile Lys Asp Leu Asp Ala Phe Arg
 260 265 270

 His Tyr Asp Gly Arg Thr Ile Ile Gln Arg Asp Asn Gly Tyr Gln Pro
 275 280 285
 Asn Tyr His Ala Val Asn Ile Val Gly Tyr Ser Asn Ala Gln Gly Val
 290 295 300
 Asp Tyr Trp Ile Val Arg Asn Ser Trp Asp Thr Asn Trp Gly Asp Asn
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67

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25

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ctcgactaa cgctgca 78

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<220>

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<213> Artificial Sequence

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<223> Primer

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<223> Primer

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ctagtagcat cttaagg 17

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<223> Primer

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<223> Mutant of DerP1

Asn Ala Glu Thr

1